

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: CHAPMAN, BARBARA
BURKE, RAE LYN
RASMUSSEN, MIRELLA EZBAN
MIKKELSON, JAN MOLLER
- (ii) TITLE OF INVENTION: PROTEIN COMPLEXES HAVING FACTOR VIII:C
ACTIVITY AND PRODUCTION THEREOF
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: REED & ROBINS
 - (B) STREET: 285 HAMILTON AVENUE, SUITE 200
 - (C) CITY: PALO ALTO
 - (D) STATE: CALIFORNIA
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 94301
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/441,943
 - (B) FILING DATE: 16-MAY-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 051,916
 - (B) FILING DATE: 19-MAY-1987
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 822,989
 - (B) FILING DATE: 27-JAN-1986
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BAROVSKY, KENNETH
 - (B) REGISTRATION NUMBER: 36,442
 - (C) REFERENCE/DOCKET NUMBER: 2300-0048.10
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 327-3400
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTAGATCT CCCGGGTCTA GATAAGTAAT

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCATTACT TATCTAGACC CGGGAGATCT

30

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGATCTCGAA TTCCCCGGGG GTACCT

26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTAGAGGTAC CCCCAGGGGAA TTCGAGATCT

30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCTCGAAT TCCCCAGGGTC TAGAGGATCC GTCGAC

36

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGGTGCAC GGATCCTCTA GACCCAGGGGA ATTCGA

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 36..47

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(46..49, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCCTCTCC AGTTGAACAT TTGTAGCAAT AAGTC ATG CAA ATA GAG CT
Met Gln Ile Glu
1

49

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gln Ile Glu
1

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTATTTGCAT GACTTATTGC TACAAATGTT CAACTGGAGA G

41

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCATGCAA

9

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCATGG

7

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	GAT	GCA	ATG	AAG	AGA	GGG	CTC	TGC	TGC	TGT	GTG	CTG	CTG	TGT	GGA	48
Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Cys	Val	Leu	Leu	Cys	Gly	
1				5				10						15		
GCA	GTC	TTC	GTT	TCG	CCC	AGC	CAG	GAA	ATC	CAT	GCC	CGA	TTC	AGA	AGA	96
Ala	Val	Phe	Val	Ser	Pro	Ser	Gln	Glu	Ile	His	Ala	Arg	Phe	Arg	Arg	
			20					25					30			
GGA	GCC	AGA	TCT	ATA	ACT	CGT	ACT	CTT	CAG	CAG	TCT	GAT				135
Gly	Ala	Arg	Ser	Ile	Thr	Arg	Thr	Leu	Gln	Gln	Ser	Asp				
			35					40				45				

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Cys	Val	Leu	Leu	Cys	Gly
1				5				10						15	
Ala	Val	Phe	Val	Ser	Pro	Ser	Gln	Glu	Ile	His	Ala	Arg	Phe	Arg	Arg
			20					25					30		
Gly	Ala	Arg	Ser	Ile	Thr	Arg	Thr	Leu	Gln	Gln	Ser	Asp			
			35					40				45			

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..135
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ATG	GAT	GCA	ATG	AAG	AGA	GGG	CTC	TGC	TGC	TGT	GTG	CTG	CTG	TGT	GGA	48
Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Cys	Val	Leu	Leu	Cys	Gly	
1				5					10					15		
GCA	GTC	TTC	GTT	TCG	CCC	AGC	CAG	GAA	ATC	CAT	GCC	CGA	TTC	AGA	AGA	96
Ala	Val	Phe	Val	Ser	Pro	Ser	Gln	Glu	Ile	His	Ala	Arg	Phe	Arg	Arg	
			20					25					30			
GGA	GCC	AGA	GAA	ATA	ACT	CGT	ACT	CTT	CAG	CAG	TCT	GAT				135
Gly	Ala	Arg	Glu	Ile	Thr	Arg	Thr	Leu	Gln	Gln	Ser	Asp				
		35				40						45				

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20 25 30
Gly Ala Arg Glu Ile Thr Arg Thr Leu Gln Gln Ser Asp
35 40 45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
GCA GTC TTC GTT TCG CCC AGC GAG ATA ACT CGT ACT CTT CAG CAG TCT	96
Ala Val Phe Val Ser Pro Ser Glu Ile Thr Arg Thr Leu Gln Gln Ser	
20 25 30	
GAT CAA GAG GAA ATT GAC TAT GAT GAT ACC	126
Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr	
35 40	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
Ala Val Phe Val Ser Pro Ser Glu Ile Thr Arg Thr Leu Gln Gln Ser	
20 25 30	
Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr	
35 40	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly	
1 5 10 15	
GCA GTC TTC GTT TCG CCC AGC CAG GAA ATC CAT GCC CGA TTC AGA AGA	96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
GAG ATA ACT CGT ACT CTT CAG CAG TCT GAT	126
Glu Ile Thr Arg Thr Leu Gln Gln Ser Asp	
35 40	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20 25 30
Glu Ile Thr Arg Thr Leu Gln Gln Ser Asp
35 40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG GAT GCA ATG AAG AGA GGG CTC TGC TGC TGT GTG CTG CTG TGT GGA 48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly
1 5 10 15
GCA GTC TTC GTT TCG CCC AGC CAG GAA ATC CAT GCC GAG ATA ACT CGT 96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Glu Ile Thr Arg
20 25 30
ACT CTT CAG CAG TCT GAT CAA GAG GAA ATT 126
Thr Leu Gln Gln Ser Asp Gln Glu Glu Ile
35 40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Cys Val Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Glu Ile Thr Arg
20 25 30
Thr Leu Gln Gln Ser Asp Gln Glu Glu Ile
35 40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Xaa Ile Xaa Arg Thr Xaa Leu Gln Xaa Asp Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Xaa Xaa Arg Glu Ile Thr Arg Thr Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Glu Ile Thr Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Xaa Gln Glu Ile
1

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG CCC TCG AGC GTC TCG TGG GGC ATC CTC CTG CTG GCA GGC CTG TGC	48
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys	
1 5 10 15	
TGC CTG GTC CCT GTC TCC CTG GCT GAG ATC ACT CGT ACT ACT CTT CAG	96
Cys Leu Val Pro Val Ser Leu Ala Glu Ile Thr Arg Thr Thr Leu Gln	
20 25 30	
TCT GAT CAA GAG GAA ATT GAC TAT GAT GAT ACC ATA TCA	135
Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys	
1 5 10 15	
Cys Leu Val Pro Val Ser Leu Ala Glu Ile Thr Arg Thr Thr Leu Gln	
20 25 30	
Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu Ile Thr Arg Thr Xaa Leu Gln Ser Asp Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc difference
(B) LOCATION: replace(1..4, "")
(D) OTHER INFORMATION: /note= "Overhang: not paired with
complimentary strand."

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGC TTC TCC CAG AAT TCT AGA CAC CCT AGC ACT AGG CAA AAG CAA TTT	48
Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe	
1 5 10 15	
AAT GCC ACC CCT CCT ACA CCA CCA ACC CCA CCA GTA CTG AAA CGC CAT	96
Asn Ala Thr Pro Pro Thr Pro Pro Thr Pro Pro Val Leu Lys Arg His	
20 25 30	
CAA CGG TGATAAG	109
Gln Arg	

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe
1 5 10 15
Asn Ala Thr Pro Thr Pro Pro Thr Pro Pro Val Leu Lys Arg His
20 25 30
Gln Arg

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(1..4, "")
- (D) OTHER INFORMATION: /note= "Overhang: not paired with complimentary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGACTTATC ACCGTTGATG GCGTTTCAGT ACTGGTGGGG TTGGTGGTGT AGGAGGGGTG 60
GCATTAAATT GCTTTTGCCT AGTGCTAGGG TGTCTAGAAT TCTGGGAGA 109

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe
1 5 10 15
Asn Ala Thr

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Pro Pro Thr Pro Pro Thr
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Pro Pro Val Leu Lys Arg His Gln Arg
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Ala Gly Leu Cys Cys
1 5 10 15

Leu Val Pro Val Ser Leu Ala
20